

i) Applicant: ISRAEL David and Wolfman, Neil M.

(ii) TITLE OF INVENTION: RECOMBINANT BONE MORPHOGENETIC PROTEIN  
HETERODIMERS, COMPOSITIONS AND METHODS OF USE

(iii) NUMBER OF SEQUENCES: 35

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
- (B) STREET: 87 CambridgePark Drive
- (C) CITY: Cambridge
- (D) STATE: MA
- (E) COUNTRY: USA
- (F) ZIP: 02140-2387

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 07/864,692
- (B) FILING DATE: 07-APR-1992
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Kapinos, Ellen J.
- (B) REGISTRATION NUMBER: 32,245
- (C) REFERENCE/DOCKET NUMBER: GI-5192A

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 617 876-1170
- (B) TELEFAX: 617 876-5851

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1607 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 356..1543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCTGACTCTA GAGTGTGTGT CAGCACTTGG CTGGGGACTT CTTGAACTTG CAGGGAGAAT	60
AACTTGCGCA CCCCACCTTG CGCCGGTGCC TTTGCCCCAG CGGAGCCTGC TTCGCCATCT	120
CCGAGCCCCA CCGCCCCTCC ACTCCTCGGC CTTGCCCCGAC ACTGAGACGC TGTTCACAGC	180

GTGAAAAGAG AGACTGCGCG GCCGGCACCG GGGAGAAGGA GGAGGCAAAG AAAAGGAAG	240
GACATTTCGGT CCTTGCGCCA GGTCTTTTGA CCAGAGTTTT TCCATGTGGA CGCTCTTTCA	300
ATGGACGTGT CCCC GCGTGC TTCTTAGACG GACTGCGGTC TCCTAAAGGT CGACC ATG	358
	Met
	1
GTG GCC GGG ACC CGC TGT CTT CTA GCG TTG CTG CTT CCC CAG GTC CTC	406
Val Ala Gly Thr Arg Cys Leu Leu Ala Leu Leu Leu Pro Gln Val Leu	
	5 10 15
CTG GGC GGC GCG GCT GGC CTC GTT CCG GAG CTG GGC CGC AGG AAG TTC	454
Leu Gly Gly Ala Ala Gly Leu Val Pro Glu Leu Gly Arg Arg Lys Phe	
	20 25 30
CGC GCG GCG TCG TCG GGC CGC CCC TCA TCC CAG CCC TCT GAC GAG GTC	502
Ala Ala Ala Ser Ser Gly Arg Pro Ser Ser Gln Pro Ser Asp Glu Val	
	35 40 45
CTG AGC GAG TTC GAG TTG CGG CTG CTC AGC ATG TTC GGC CTG AAA CAG	550
Leu Ser Glu Phe Glu Leu Arg Leu Leu Ser Met Phe Gly Leu Lys Gln	
	50 55 60 65
AGA CCC ACC CCC AGC AGG GAC GCC GTG GTG CCC CCC TAC ATG CTA GAC	598
Arg Pro Thr Pro Ser Arg Asp Ala Val Val Pro Pro Tyr Met Leu Asp	
	70 75 80
CTG TAT CGC AGG CAC TCA GGT CAG CCG GGC TCA CCC GCC CCA GAC CAC	646
Leu Tyr Arg Arg His Ser Gly Gln Pro Gly Ser Pro Ala Pro Asp His	
	85 90 95
CGG TTG GAG AGG GCA GCC AGC CGA GCC AAC ACT GTG CGC AGC TTC CAC	694
Arg Leu Glu Arg Ala Ala Ser Arg Ala Asn Thr Val Arg Ser Phe His	
	100 105 110
CAT GAA GAA TCT TTG GAA GAA CTA CCA GAA ACG AGT GGG AAA ACA ACC	742
His Glu Glu Ser Leu Glu Glu Leu Pro Glu Thr Ser Gly Lys Thr Thr	
	115 120 125
CGG AGA TTC TTC TTT AAT TTA AGT TCT ATC CCC ACG GAG GAG TTT ATC	790
Arg Arg Phe Phe Phe Asn Leu Ser Ser Ile Pro Thr Glu Glu Phe Ile	
	130 135 140 145
ACC TCA GCA GAG CTT CAG GTT TTC CGA GAA CAG ATG CAA GAT GCT TTA	838
Thr Ser Ala Glu Leu Gln Val Phe Arg Glu Gln Met Gln Asp Ala Leu	
	150 155 160
GGA AAC AAT AGC AGT TTC CAT CAC CGA ATT AAT ATT TAT GAA ATC ATA	886
Gly Asn Asn Ser Ser Phe His His Arg Ile Asn Ile Tyr Glu Ile Ile	
	165 170 175
AAA CCT GCA ACA GCC AAC TCG AAA TTC CCC GTG ACC AGA CTT TTG GAC	934
Lys Pro Ala Thr Ala Asn Ser Lys Phe Pro Val Thr Arg Leu Leu Asp	
	180 185 190
ACC AGG TTG GTG AAT CAG AAT GCA AGC AGG TGG GAA ACT TTT GAT GTC	982
Thr Arg Leu Val Asn Gln Asn Ala Ser Arg Trp Glu Thr Phe Asp Val	
	195 200 205

ACC CCC GCT GTG ATG CGG TGG ACT TCA CAG GGA CAC GCC AAC CAT GGA	1030
Thr Pro Ala Val Met Arg Trp Thr Ala Gln Gly His Ala Asn His Gly	
210 215 220 225	
TTC GTG GTG GAA GTG GCC CAC TTG GAG GAG AAA CAA GGT GTC TCC AAG	1078
Phe Val Val Glu Val Ala His Leu Glu Glu Lys Gln Gly Val Ser Lys	
230 235 240	
AGA CAT GTT AGG ATA AGC AGG TCT TTG CAC CAA GAT GAA CAC AGC TGG	1126
Arg His Val Arg Ile Ser Arg Ser Leu His Gln Asp Glu His Ser Trp	
245 250 255	
TCA CAG ATA AGG CCA TTG CTA GTA ACT TTT GGC CAT GAT GGA AAA GGG	1174
Ser Gln Ile Arg Pro Leu Leu Val Thr Phe Gly His Asp Gly Lys Gly	
260 265 270	
CAT CCT CTC CAC AAA AGA GAA AAA CGT CAA GCC AAA CAC AAA CAG CGG	1222
His Pro Leu His Lys Arg Glu Lys Arg Gln Ala Lys His Lys Gln Arg	
275 280 285	
AAA CGC CTT AAG TCC AGC TGT AAG AGA CAC CCT TTG TAC GTG GAC TTC	1270
Lys Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu Tyr Val Asp Phe	
290 295 300 305	
AGT GAC GTG GGG TGG AAT GAC TGG ATT GTG GCT CCC CCG GGG TAT CAC	1318
Ser Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr His	
310 315 320	
GCC TTT TAC TGC CAC GGA GAA TGC CCT TTT CCT CTG GCT GAT CAT CTG	1366
Ala Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His Leu	
325 330 335	
AAC TCC ACT AAT CAT GCC ATT GTT CAG ACG TTG GTC AAC TCT GTT AAC	1414
Asn Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn	
340 345 350	
TCT AAG ATT CCT AAG GCA TGC TGT GTC CCG ACA GAA CTC AGT GCT ATC	1462
Ser Lys Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile	
355 360 365	
TCG ATG CTG TAC CTT GAC GAG AAT GAA AAG GTT GTA TTA AAG AAC TAT	1510
Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys Val Val Leu Lys Asn Tyr	
370 375 380 385	
CAG GAC ATG GTT GTG GAG GGT TGT GGG TGT CGC TAGTACAGCA AAATTAAATA	1563
Gln Asp Met Val Val Glu Gly Cys Gly Cys Arg	
390 395	
CATAAATATA TATATATATA TATATTTTAG AAAAAAGAAA AAAA	1607

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION SEQ ID NO:2:

Met Val Ala Gly Thr Arg Cys Leu Leu Ala Leu Leu Leu Pro Gln Val  
1 5 10 15  
Leu Leu Gly Gly Ala Ala Gly Leu Val Pro Glu Leu Gly Arg Arg Lys  
20 25 30  
Phe Ala Ala Ala Ser Ser Gly Arg Pro Ser Ser Gln Pro Ser Asp Glu  
35 40 45  
Val Leu Ser Glu Phe Glu Leu Arg Leu Leu Ser Met Phe Gly Leu Lys  
50 55 60  
Gln Arg Pro Thr Pro Ser Arg Asp Ala Val Val Pro Pro Tyr Met Leu  
65 70 75 80  
Asp Leu Tyr Arg Arg His Ser Gly Gln Pro Gly Ser Pro Ala Pro Asp  
85 90 95  
His Arg Leu Glu Arg Ala Ala Ser Arg Ala Asn Thr Val Arg Ser Phe  
100 105 110  
His His Glu Glu Ser Leu Glu Glu Leu Pro Glu Thr Ser Gly Lys Thr  
115 120 125  
Thr Arg Arg Phe Phe Phe Asn Leu Ser Ser Ile Pro Thr Glu Glu Phe  
130 135 140  
Ile Thr Ser Ala Glu Leu Gln Val Phe Arg Glu Gln Met Gln Asp Ala  
145 150 155 160  
Leu Gly Asn Asn Ser Ser Phe His His Arg Ile Asn Ile Tyr Glu Ile  
165 170 175  
Ile Lys Pro Ala Thr Ala Asn Ser Lys Phe Pro Val Thr Arg Leu Leu  
180 185 190  
Asp Thr Arg Leu Val Asn Gln Asn Ala Ser Arg Trp Glu Thr Phe Asp  
195 200 205  
Val Thr Pro Ala Val Met Arg Trp Thr Ala Gln Gly His Ala Asn His  
210 215 220  
Gly Phe Val Val Glu Val Ala His Leu Glu Glu Lys Gln Gly Val Ser  
225 230 235 240  
Lys Arg His Val Arg Ile Ser Arg Ser Leu His Gln Asp Glu His Ser  
245 250 255  
Trp Ser Gln Ile Arg Pro Leu Leu Val Thr Phe Gly His Asp Gly Lys  
260 265 270  
Gly His Pro Leu His Lys Arg Glu Lys Arg Gln Ala Lys His Lys Gln  
275 280 285  
Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu Tyr Val Asp  
290 295 300  
Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr

His Ala Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His  
325330335

Leu Asn Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val  
340345350

Asn Ser Lys Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala  
355360365

Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys Val Val Leu Lys Asn  
370375380

Tyr Gln Asp Met Val Val Glu Gly Cys Gly Cys Arg  
385390395

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1954 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
- (B) LOCATION: 403..1626

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCTAGAGGG CAGAGGAGGA GGGAGGGAGG GAAGGAGCGC GGAGCCCGGC CCGGAAGCTA60

GGTGAGTGTG GCATCCGAGC TGAGGGACGC GAGCCTGAGA CGCCGCTGCT GCTCCGGCTG120

AGTATCTAGC TTGTCTCCCC GATGGGATTC CCGTCCAAGC TATCTCGAGC CTGCAGCGCC180

ACAGTCCCCG GCCCTCGCCC AGGTTCACTG CAACCGTTCA GAGGTCCCCA GGAGCTGCTG240

CTGGCGAGCC CGCTACTGCA GGGACCTATG GAGCCATTCC GTAGTGCCAT CCCGAGCAAC300

GCACTGCTGC AGCTTCCCTG AGCCTTTCCA GCAAGTTTGT TCAAGATTGG CTGTCAAGAA360

TCATGGACTG TTATTATATG CCTTGTTTTC TGTCAAGACA CC ATG ATT CCT GGT414

Met Ile Pro Gly1

AAC CGA ATG CTG ATG GTC GTT TTA TTA TGC CAA GTC CTG CTA GGA GGC462

Asn Arg Met Leu Met Val Val Leu Leu Cys Gln Val Leu Leu Gly Gly510

510253035

GCG AGC CAT GCT AGT TTG ATA CCT GAG ACG GGG AAG AAA AAA GTC GCC510

Ala Ser His Ala Ser Leu Ile Pro Glu Thr Gly Lys Lys Lys Val Ala

253035

GAG ATT CAG GGC CAC GCG GGA GGA CGC CGC TCA GGG CAG AGC CAT GAG558

Glu	Ile	Gln	Gly	His	Ala	Gly	Gly	Arg	Arg	Ser	Gly	Gln	Ser	His	Glu		
			40					45					50				
CTC	CTG	CGG	GAC	TTC	GAG	GCG	ACA	CTT	CTG	CAG	ATG	TTT	GGG	CTG	CGC	606	
Leu	Leu	Arg	Asp	Phe	Glu	Ala	Thr	Leu	Leu	Gln	Met	Phe	Gly	Leu	Arg		
		55					60					65					
CGC	CGC	CCG	CAG	CCT	AGC	AAG	AGT	GCC	GTC	ATT	CCG	GAC	TAC	ATG	CGG	654	
Arg	Arg	Pro	Gln	Pro	Ser	Lys	Ser	Ala	Val	Ile	Pro	Asp	Tyr	Met	Arg		
		70				75					80						
GAT	CTT	TAC	CGG	CTT	CAG	TCT	GGG	GAG	GAG	GAG	GAA	GAG	CAG	ATC	CAC	702	
Asp	Leu	Tyr	Arg	Leu	Gln	Ser	Gly	Glu	Glu	Glu	Glu	Glu	Gln	Ile	His		
					90					95					100		
AGC	ACT	GGT	CTT	GAG	TAT	CCT	GAG	CGC	CCG	GCC	AGC	CGG	GCC	AAC	ACC	750	
Ser	Thr	Gly	Leu	Glu	Tyr	Pro	Glu	Arg	Pro	Ala	Ser	Arg	Ala	Asn	Thr		
				105					110					115			
GTG	AGG	AGC	TTC	CAC	CAC	GAA	GAA	CAT	CTG	GAG	AAC	ATC	CCA	GGG	ACC	798	
Val	Arg	Ser	Phe	His	His	Glu	Glu	His	Leu	Glu	Asn	Ile	Pro	Gly	Thr		
			120					125					130				
AGT	GAA	AAC	TCT	GCT	TTT	CGT	TTC	CTC	TTT	AAC	CTC	AGC	AGC	ATC	CCT	846	
Ser	Glu	Asn	Ser	Ala	Phe	Arg	Phe	Leu	Phe	Asn	Leu	Ser	Ser	Ile	Pro		
		135					140					145					
GAG	AAC	GAG	GTG	ATC	TCC	TCT	GCA	GAG	CTT	CGG	CTC	TTC	CGG	GAG	CAG	894	
Glu	Asn	Glu	Val	Ile	Ser	Ser	Ala	Glu	Leu	Arg	Leu	Phe	Arg	Glu	Gln		
		150				155					160						
GTG	GAC	CAG	GGC	CCT	GAT	TGG	GAA	AGG	GGC	TTC	CAC	CGT	ATA	AAC	ATT	942	
Val	Asp	Gln	Gly	Pro	Asp	Trp	Glu	Arg	Gly	Phe	His	Arg	Ile	Asn	Ile		
	165				170				175					180			
TAT	GAG	GTT	ATG	AAG	CCC	CCA	GCA	GAA	GTG	GTG	CCT	GGG	CAC	CTC	ATC	990	
Tyr	Glu	Val	Met	Lys	Pro	Pro	Ala	Glu	Val	Val	Pro	Gly	His	Leu	Ile		
				185					190					195			
ACA	CGA	CTA	CTG	GAC	ACG	AGA	CTG	GTC	CAC	CAC	AAT	GTG	ACA	CGG	TGG	1038	
Thr	Arg	Leu	Leu	Asp	Thr	Arg	Leu	Val	His	His	Asn	Val	Thr	Arg	Trp		
			200					205					210				
GAA	ACT	TTT	GAT	GTG	AGC	CCT	GCG	GTC	CTT	CGC	TGG	ACC	CGG	GAG	AAG	1086	
Glu	Thr	Phe	Asp	Val	Ser	Pro	Ala	Val	Leu	Arg	Trp	Thr	Arg	Glu	Lys		
		215					220					225					
CAG	CCA	AAC	TAT	GGG	CTA	GCC	ATT	GAG	GTG	ACT	CAC	CTC	CAT	CAG	ACT	1134	
Gln	Pro	Asn	Tyr	Gly	Leu	Ala	Ile	Glu	Val	Thr	His	Leu	His	Gln	Thr		
		230				235					240						
CGG	ACC	CAC	CAG	GGC	CAG	CAT	GTC	AGG	ATT	AGC	CGA	TCG	TTA	CCT	CAA	1182	
Arg	Thr	His	Gln	Gly	Gln	His	Val	Arg	Ile	Ser	Arg	Ser	Leu	Pro	Gln		
				250					255						260		
GGG	AGT	GGG	AAT	TGG	GCC	CAG	CTC	CGG	CCC	CTC	CTG	GTC	ACC	TTT	GGC	1230	
Gly	Ser	Gly	Asn	Trp	Ala	Gln	Leu	Arg	Pro	Leu	Leu	Val	Thr	Phe	Gly		
				265					270					275			
CAT	GAT	GGC	CGG	GGC	CAT	GCC	TTG	ACC	CGA	CGC	CGG	AGG	GCC	AAG	CGT	1278	

His Asp Gly Arg Gly His Ala Leu	280	285	290	Arg Arg Arg Arg Ala Lys Arg	
AGC CCT AAG CAT CAC TCA CAG CGG GCC AGG AAG AAG AAT AAG AAC TGC					1326
Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys Asn Lys Asn Cys	295	300	305		
CGG CGC CAC TCG CTC TAT GTG GAC TTC AGC GAT GTG GGC TGG AAT GAC					1374
Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp	310	315	320		
TGG ATT GTG GCC CCA CCA GGC TAC CAG GCC TTC TAC TGC CAT GGG GAC					1422
Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His Gly Asp	325	330	335	340	
TGC CCC TTT CCA CTG GCT GAC CAC CTC AAC TCA ACC AAC CAT GCC ATT					1470
Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile	345	350	355		
GTG CAG ACC CTG GTC AAT TCT GTC AAT TCC AGT ATC CCC AAA GCC TGT					1518
Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile Pro Lys Ala Cys	360	365	370		
TGT GTG CCC ACT GAA CTG AGT GCC ATC TCC ATG CTG TAC CTG GAT GAG					1566
Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu	375	380	385		
TAT GAT AAG GTG GTA CTG AAA AAT TAT CAG GAG ATG GTA GTA GAG GGA					1614
Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met Val Val Glu Gly	390	395	400		
TGT GGG TGC CGC TGAGATCAGG CAGTCCTTGA GGATAGACAG ATATACACAC					1666
Cys Gly Cys Arg	405				
CACACACACA CACCACATAC ACCACACACA CACGTTCCCA TCCAATCACC CACACACTAC					1726
ACAGACTGCT TCCTTATAGC TGGACTTTTA TTTAAAAAAA AAAAAAAAAA AATGGAAAAA					1786
ATCCCTAAAC ATTCACCTTG ACCTTATTTA TGACTTTACG TGCAAATGTT TTGACCATAT					1846
TGATCATATA TTTTGACAAA ATATATTTAT AACTACGTAT TAAAAGAAAA AAATAAAATG					1906
AGTCATTATT TTAAAAAAA AAAAAAAACT CTAGAGTCGA CGGAATTC					1954

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ile	Pro	Gly	Asn	Arg	Met	Leu	Met	Val	Val	Leu	Leu	Cys	Gln	Val
1				5					10					15	

Leu Leu Gly Gly Ala Ser His Ala Ser Leu Ile Pro Glu Thr Gly Lys  
 20 25 30  
 Lys Lys Val Ala Glu Ile Gln Gly His Ala Gly Gly Arg Arg Ser Gly  
 35 40 45  
 Gln Ser His Glu Leu Leu Arg Asp Phe Glu Ala Thr Leu Leu Gln Met  
 50 55 60  
 Phe Gly Leu Arg Arg Arg Pro Gln Pro Ser Lys Ser Ala Val Ile Pro  
 65 70 75 80  
 Asp Tyr Met Arg Asp Leu Tyr Arg Leu Gln Ser Gly Glu Glu Glu Glu  
 85 90 95  
 Glu Gln Ile His Ser Thr Gly Leu Glu Tyr Pro Glu Arg Pro Ala Ser  
 100 105 110  
 Arg Ala Asn Thr Val Arg Ser Phe His His Glu Glu His Leu Glu Asn  
 115 120 125  
 Ile Pro Gly Thr Ser Glu Asn Ser Ala Phe Arg Phe Leu Phe Asn Leu  
 130 135 140  
 Ser Ser Ile Pro Glu Asn Glu Val Ile Ser Ser Ala Glu Leu Arg Leu  
 145 150 155 160  
 Phe Arg Glu Gln Val Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His  
 165 170 175  
 Arg Ile Asn Ile Tyr Glu Val Met Lys Pro Pro Ala Glu Val Val Pro  
 180 185 190  
 Gly His Leu Ile Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn  
 195 200 205  
 Val Thr Arg Trp Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp  
 210 215 220  
 Thr Arg Glu Lys Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His  
 225 230 235 240  
 Leu His Gln Thr Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg  
 245 250 255  
 Ser Leu Pro Gln Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu  
 260 265 270  
 Val Thr Phe Gly His Asp Gly Arg Gly His Ala Leu Thr Arg Arg Arg  
 275 280 285  
 Arg Ala Lys Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys  
 290 295 300  
 Asn Lys Asn Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val  
 305 310 315 320  
 Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr  
 325 330 335



Cys His Gly Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr  
 340 345 350  
 Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile  
 355 360 365  
 Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu  
 370 375 380  
 Tyr Leu Asp Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met  
 385 390 395 400  
 Val Val Glu Gly Cys Gly Cys Arg  
 405

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 97..1389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTGACCGAGC GGCGCGGACG GCCGCCTGCC CCCTCTGCCA CCTGGGGCGG TCGGGGCCCG	60
GAGCCCGGAG CCCGGGTAGC GCGTAGAGCC GGCGCG ATG CAC GTG CGC TCA CTG	114
Met His Val Arg Ser Leu	
1 5	
CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA CCC CTG TTC	162
Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala Pro Leu Phe	
10 15 20	
CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC GAG GTG CAC	210
Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn Glu Val His	
25 30 35	
TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG CGG GAG ATG	258
Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg Arg Glu Met	
40 45 50	
CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC CCG CGC CCG	306
Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg Pro Arg Pro	
55 60 65 70	
CAC CTC CAG GGC AAG CAC AAC TCG GCA CCC ATG TTC ATG CTG GAC CTG	354
His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met Leu Asp Leu	
75 80 85	
TAC AAC GCC ATG GCG GTG GAG GAG GGC GGC GGC CCC GGC GGC CAG GGC	402

Tyr	Asn	Ala	Met	Ala	Val	Glu	Gln	Gly	Gly	Pro	Gly	Gly	Gln	Gly		
			90				95			100						
TTC	TCC	TAC	CCC	TAC	AAG	GCC	GTC	TTC	AGT	ACC	CAG	GGC	CCC	CCT	CTG	450
Phe	Ser	Tyr	Pro	Tyr	Lys	Ala	Val	Phe	Ser	Thr	Gln	Gly	Pro	Pro	Leu	
			105				110			115						
GCC	AGC	CTG	CAA	GAT	AGC	CAT	TTC	CTC	ACC	GAC	GCC	GAC	ATG	GTC	ATG	498
Ala	Ser	Leu	Gln	Asp	Ser	His	Phe	Leu	Thr	Asp	Ala	Asp	Met	Val	Met	
			120				125			130						
AGC	TTC	GTC	AAC	CTC	GTG	GAA	CAT	GAC	AAG	GAA	TTC	TTC	CAC	CCA	CGC	546
Ser	Phe	Val	Asn	Leu	Val	Glu	His	Asp	Lys	Glu	Phe	Phe	His	Pro	Arg	
			135				140			145			150			
TAC	CAC	CAT	CGA	GAG	TTC	CGG	TTT	GAT	CTT	TCC	AAG	ATC	CCA	GAA	GGG	594
Tyr	His	His	Arg	Glu	Phe	Arg	Phe	Asp	Leu	Ser	Lys	Ile	Pro	Glu	Gly	
			155				160						165			
GAA	GCT	GTC	ACG	GCA	GCC	GAA	TTC	CGG	ATC	TAC	AAG	GAC	TAC	ATC	CGG	642
Glu	Ala	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile	Tyr	Lys	Asp	Tyr	Ile	Arg	
			170				175			180						
GAA	CGC	TTC	GAC	AAT	GAG	ACG	TTC	CGG	ATC	AGC	GTT	TAT	CAG	GTG	CTC	690
Glu	Arg	Phe	Asp	Asn	Glu	Thr	Phe	Arg	Ile	Ser	Val	Tyr	Gln	Val	Leu	
			185				190			195						
CAG	GAG	CAC	TTG	GGC	AGG	GAA	TCG	GAT	CTC	TTC	CTG	CTC	GAC	AGC	CGT	738
Gln	Glu	His	Leu	Gly	Arg	Glu	Ser	Asp	Leu	Phe	Leu	Leu	Asp	Ser	Arg	
			200				205			210						
ACC	CTC	TGG	GCC	TCG	GAG	GAG	GGC	TGG	CTG	GTG	TTT	GAC	ATC	ACA	GCC	786
Thr	Leu	Trp	Ala	Ser	Glu	Glu	Gly	Trp	Leu	Val	Phe	Asp	Ile	Thr	Ala	
			215				220			225			230			
ACC	AGC	AAC	CAC	TGG	GTG	GTC	AAT	CCG	CGG	CAC	AAC	CTG	GGC	CTG	CAG	834
Thr	Ser	Asn	His	Trp	Val	Val	Asn	Pro	Arg	His	Asn	Leu	Gly	Leu	Gln	
			235				240			245						
CTC	TCG	GTG	GAG	ACG	CTG	GAT	GGG	CAG	AGC	ATC	AAC	CCC	AAG	TTG	GCG	882
Leu	Ser	Val	Glu	Thr	Leu	Asp	Gly	Gln	Ser	Ile	Asn	Pro	Lys	Leu	Ala	
			250				255			260						
GGC	CTG	ATT	GGG	CGG	CAC	GGG	CCC	CAG	AAC	AAG	CAG	CCC	TTC	ATG	GTG	930
Gly	Leu	Ile	Gly	Arg	His	Gly	Pro	Gln	Asn	Lys	Gln	Pro	Phe	Met	Val	
			265				270			275						
GCT	TTC	TTC	AAG	GCC	ACG	GAG	GTC	CAC	TTC	CGC	AGC	ATC	CGG	TCC	ACG	978
Ala	Phe	Phe	Lys	Ala	Thr	Glu	Val	His	Phe	Arg	Ser	Ile	Arg	Ser	Thr	
			280				285			290						
GGG	AGC	AAA	CAG	CGC	AGC	CAG	AAC	CGC	TCC	AAG	ACG	CCC	AAG	AAC	CAG	1026
Gly	Ser	Lys	Gln	Arg	Ser	Gln	Asn	Arg	Ser	Lys	Thr	Pro	Lys	Asn	Gln	
			295				300			305			310			
GAA	GCC	CTG	CGG	ATG	GCC	AAC	GTG	GCA	GAG	AAC	AGC	AGC	AGC	GAC	CAG	1074
Glu	Ala	Leu	Arg	Met	Ala	Asn	Val									

Arg	Gln	Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	Arg	Asp	Leu	
			330					335					340			
GGC	TGG	CAG	GAC	TGG	ATC	ATC	GCG	CCT	GAA	GGC	TAC	GCC	GCC	TAC	TAC	1170
Gly	Trp	Gln	Asp	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala	Ala	Tyr	Tyr	
		345					350					355				
TGT	GAG	GGG	GAG	TGT	GCC	TTC	CCT	CTG	AAC	TCC	TAC	ATG	AAC	GCC	ACC	1218
Cys	Glu	Gly	Glu	Cys	Ala	Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn	Ala	Thr	
	360					365					370					
AAC	CAC	GCC	ATC	GTG	CAG	ACG	CTG	GTC	CAC	TTC	ATC	AAC	CCG	GAA	ACG	1266
Asn	His	Ala	Ile	Val	Gln	Thr	Leu	Val	His	Phe	Ile	Asn	Pro	Glu	Thr	
375					380					385					390	
GTG	CCC	AAG	CCC	TGC	TGT	GCG	CCC	ACG	CAG	CTC	AAT	GCC	ATC	TCC	GTC	1314
Val	Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln	Leu	Asn	Ala	Ile	Ser	Val	
				395					400					405		
CTC	TAC	TTC	GAT	GAC	AGC	TCC	AAC	GTC	ATC	CTG	AAG	AAA	TAC	AGA	AAC	1362
Leu	Tyr	Phe	Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys	Lys	Tyr	Arg	Asn	
			410					415					420			
ATG	GTG	GTC	CGG	GCC	TGT	GGC	TGC	CAC	TAGCTCCTCC GAGAATTCAG							1409
Met	Val	Val	Arg	Ala	Cys	Gly	Cys	His								
		425				430										
ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTC																1448

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	His	Val	Arg	Ser	Leu	Arg	Ala	Ala	Ala	Pro	His	Ser	Phe	Val	Ala	
1				5					10					15		
Leu	Trp	Ala	Pro	Leu	Phe	Leu	Leu	Arg	Ser	Ala	Leu	Ala	Asp	Phe	Ser	
			20					25					30			
Leu	Asp	Asn	Glu	Val	His	Ser	Ser	Phe	Ile	His	Arg	Arg	Leu	Arg	Ser	
		35					40					45				
Gln	Glu	Arg	Arg	Glu	Met	Gln	Arg	Glu	Ile	Leu	Ser	Ile	Leu	Gly	Leu	
	50					55					60					
Pro	His	Arg	Pro	Arg	Pro	His	Leu	Gln	Gly	Lys	His	Asn	Ser	Ala	Pro	
	65				70					75					80	
Met	Phe	Met	Leu	Asp	Leu	Tyr	Asn	Ala	Met	Ala	Val	Glu	Glu	Gly	Gly	
			85					90						95		
Gly	Pro	Gly	Gly	Gln	Gly	Phe	Ser	Tyr	Pro	Tyr	Lys	Ala	Val	Phe	Ser	

Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr  
 115 120 125  
 Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys  
 130 135 140  
 Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu  
 145 150 155 160  
 Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile  
 165 170 175  
 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile  
 180 185 190  
 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu  
 195 200 205  
 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu  
 210 215 220  
 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg  
 225 230 235 240  
 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser  
 245 250 255  
 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn  
 260 265 270  
 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe  
 275 280 285  
 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser  
 290 295 300  
 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu  
 305 310 315 320  
 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr  
 325 330 335  
 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu  
 340 345 350  
 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn  
 355 360 365  
 Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His  
 370 375 380  
 Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln  
 385 390 395 400  
 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile  
 405 410 415  
 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (F) TISSUE TYPE: Human placenta

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Stratagene catalog #936203 Human placenta cDNA library
- (B) CLONE: BMP6C35

## (viii) POSITION IN GENOME:

- (C) UNITS: bp

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 160..1701

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1282..1698

## (ix) FEATURE:

- (A) NAME/KEY: mRNA
- (B) LOCATION: 1..2923

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGACCATGAG AGATAAGGAC TGAGGGCCAG GAAGGGGAAG CGAGCCCGCC GAGAGGTGGC	60
GGGGACTGCT CACGCCAAGG GCCACAGCGG CCGCGCTCCG GCCTCGCTCC GCCGCTCCAC	120
GCCTCGCGGG ATCCGCGGGG GCAGCCCGGC CGGGCGGGG ATG CCG GGG CTG GGG	174
Met Pro Gly Leu Gly	
-374 -370	
CGG AGG GCG CAG TGG CTG TGC TGG TGG TGG GGG CTG CTG TGC AGC TGC	222
Arg Arg Ala Gln Trp Leu Cys Trp Trp Trp Gly Leu Leu Cys Ser Cys	
-365 -360 -355	
TGC GGG CCC CCG CCG CTG CCG CCG CCC TTG CCC GCT GCC GCG GCC GCC	270
Cys Gly Pro Pro Pro Leu Arg Pro Pro Leu Pro Ala Ala Ala Ala Ala	
-350 -345 -340	
GCC GCC GGG GGG CAG CTG CTG GGG GAC GGC GGG AGC CCC GGC CGC ACG	318
Ala Ala Gly Gly Gln Leu Leu Gly Asp Gly Gly Ser Pro Gly Arg Thr	
-335 -330 -325	

GAG CAG CCG CCG CCG TCG CCG CAG TCC TCC TCG GGC TTC CTG TAC CGG Glu Gln Pro Pro Pro Ser Pro Gln Ser Ser Ser Gly Phe Leu Tyr Arg -320 -315 -310	366
CGG CTC AAG ACG CAG GAG AAG CGG GAG ATG CAG AAG GAG ATC TTG TCG Arg Leu Lys Thr Gln Glu Lys Arg Glu Met Gln Lys Glu Ile Leu Ser -305 -300 -295 -290	414
GTG CTG GGG CTC CCG CAC CGG CCC CGG CCC CTG CAC GGC CTC CAA CAG Val Leu Gly Leu Pro His Arg Pro Arg Pro Leu His Gly Leu Gln Gln -285 -280 -275	462
CCG CAG CCC CCG GCG CTC CGG CAG CAG GAG GAG CAG CAG CAG CAG CAG Pro Gln Pro Pro Ala Leu Arg Gln Gln Glu Glu Gln Gln Gln Gln Gln -270 -265 -260	510
CAG CTG CCT CGC GGA GAG CCC CCT CCC GGG CGA CTG AAG TCC GCG CCC Gln Leu Pro Arg Gly Glu Pro Pro Pro Gly Arg Leu Lys Ser Ala Pro -255 -250 -245	558
CTC TTC ATG CTG GAT CTG TAC AAC GCC CTG TCC GCC GAC AAC GAC GAG Leu Phe Met Leu Asp Leu Tyr Asn Ala Leu Ser Ala Asp Asn Asp Glu -240 -235 -230	606
GAC GGG GCG TCG GAG GGG GAG AGG CAG CAG TCC TGG CCC CAC GAA GCA Asp Gly Ala Ser Glu Gly Glu Arg Gln Gln Ser Trp Pro His Glu Ala -225 -220 -215 -210	654
GCC AGC TCG TCC CAG CGT CGG CAG CCG CCC CGG GGC GCC GCG CAC CCG Ala Ser Ser Ser Gln Arg Arg Gln Pro Pro Pro Gly Ala Ala His Pro -205 -200 -195	702
CTC AAC CGC AAG AGC CTT CTG GCC CCC GGA TCT GGC AGC GGC GGC GCG Leu Asn Arg Lys Ser Leu Leu Ala Pro Gly Ser Gly Ser Gly Gly Ala -190 -185 -180	750
TCC CCA CTG ACC AGC GCG CAG GAC AGC GCC TTC CTC AAC GAC GCG GAC Ser Pro Leu Thr Ser Ala Gln Asp Ser Ala Phe Leu Asn Asp Ala Asp -175 -170 -165	798
ATG GTC ATG AGC TTT GTG AAC CTG GTG GAG TAC GAC AAG GAG TTC TCC Met Val Met Ser Phe Val Asn Leu Val Glu Tyr Asp Lys Glu Phe Ser -160 -155 -150	846
CCT CGT CAG CGA CAC CAC AAA GAG TTC AAG TTC AAC TTA TCC CAG ATT Pro Arg Gln Arg His His Lys Glu Phe Lys Phe Asn Leu Ser Gln Ile -145 -140 -135 -130	894
CCT GAG GGT GAG GTG GTG ACG GCT GCA GAA TTC CGC ATC TAC AAG GAC Pro Glu Gly Glu Val Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp -125 -120 -115	942
TGT GTT ATG GGG AGT TTT AAA AAC CAA ACT TTT CTT ATC AGC ATT TAT Cys Val Met Gly Ser Phe Lys Asn Gln Thr Phe Leu Ile Ser Ile Tyr -110 -105 -100	990
CAA GTC TTA CAG GAG CAT CAG CAC AGA GAC TCT GAC CTG TTT TTG TTG Gln Val Leu Gln Glu His Gln His Arg Asp Ser Asp Leu Phe Leu Leu -95 -90 -85	1038

GAC ACC CGT GTA GTA TGG GCC TCA GAA GAA GGC TGG CTG GAA TTT GAC Asp Thr Arg Val Val Trp Ala Ser Glu Glu Gly Trp Leu Glu Phe Asp -80 -75 -70	1086
ATC ACG GCC ACT AGC AAT CTG TGG GTT GTG ACT CCA CAG CAT AAC ATG Ile Thr Ala Thr Ser Asn Leu Trp Val Val Thr Pro Gln His Asn Met -65 -60 -55 -50	1134
GGG CTT CAG CTG AGC GTG GTG ACA AGG GAT GGA GTC CAC GTC CAC CCC Gly Leu Gln Leu Ser Val Val Thr Arg Asp Gly Val His Val His Pro -45 -40 -35	1182
CGA GCC GCA GGC CTG GTG GGC AGA GAC GGC CCT TAC GAT AAG CAG CCC Arg Ala Ala Gly Leu Val Gly Arg Asp Gly Pro Tyr Asp Lys Gln Pro -30 -25 -20	1230
TTC ATG GTG GCT TTC TTC AAA GTG AGT GAG GTC CAC GTG CGC ACC ACC Phe Met Val Ala Phe Phe Lys Val Ser Glu Val His Val Arg Thr Thr -15 -10 -5	1278
AGG TCA GCC TCC AGC CGG CGC CGA CAA CAG AGT CGT AAT CGC TCT ACC Arg Ser Ala Ser Ser Arg Arg Arg Gln Gln Ser Arg Asn Arg Ser Thr 1 5 10 15	1326
CAG TCC CAG GAC GTG GCG CGG GTC TCC AGT GCT TCA GAT TAC AAC AGC Gln Ser Gln Asp Val Ala Arg Val Ser Ser Ala Ser Asp Tyr Asn Ser 20 25 30	1374
AGT GAA TTG AAA ACA GCC TGC AGG AAG CAT GAG CTG TAT GTG AGT TTC Ser Glu Leu Lys Thr Ala Cys Arg Lys His Glu Leu Tyr Val Ser Phe 35 40 45	1422
CAA GAC CTG GGA TGG CAG GAC TGG ATC ATT GCA CCC AAG GGC TAT GCT Gln Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Lys Gly Tyr Ala 50 55 60	1470
GCC AAT TAC TGT GAT GGA GAA TGC TCC TTC CCA CTC AAC GCA CAC ATG Ala Asn Tyr Cys Asp Gly Glu Cys Ser Phe Pro Leu Asn Ala His Met 65 70 75	1518
AAT GCA ACC AAC CAC GCG ATT GTG CAG ACC TTG GTT CAC CTT ATG AAC Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Leu Met Asn 80 85 90 95	1566
CCC GAG TAT GTC CCC AAA CCG TGC TGT GCG CCA ACT AAG CTA AAT GCC Pro Glu Tyr Val Pro Lys Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala 100 105 110	1614
ATC TCG GTT CTT TAC TTT GAT GAC AAC TCC AAT GTC ATT CTG AAA AAA Ile Ser Val Leu Tyr Phe Asp Asp Asn Ser Asn Val Ile Leu Lys Lys 115 120 125	1662
TAC AGG AAT ATG GTT GTA AGA GCT TGT GGA TGC CAC TAACTCGAAA Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His 130 135 140	1708
CCAGATGCTG GGGACACACA TTCTGCCTTG GATTCCTAGA TTACATCTGC CTAAAAAAA	1768
CACGGAAGCA CAGTTGGAGG TGGGACGATG AGACTTTGAA ACTATCTCAT GCCAGTGCCT	1828

TATTACCCAG GAAGATTTTA AAGGACCTCA TTAATAATTT GCTCACTTGG TAAATGACGT	1888
GAGTAGTTGT TGGTCTGTAG CAAGCTGAGT TTGGATGTCT GTAGCATAAG GTCTGGTAAC	1948
TGCAGAAACA TAACCGTGAA GCTCTTCCTA CCCTCCTCCC CCAAAAACCC ACCAAAATTA	2008
GTTTTAGCTG TAGATCAAGC TATTTGGGGT GTTTGTTAGT AAATAGGGAA AATAATCTCA	2068
AAGGAGTTAA ATGTATTCTT GGCTAAAGGA TCAGCTGGTT CAGTACTGTC TATCAAAGGT	2128
AGATTTTACA GAGAACAGAA ATCGGGGAAG TGGGGGGAAC GCCTCTGTTC AGTTCATTCC	2188
CAGAAGTCCA CAGGACGCAC AGCCCAGGCC ACAGCCAGGG CTCCACGGGG CGCCCTTGTC	2248
TCAGTCATTG CTGTTGTATG TTCGTGCTGG AGTTTTGTTG GTGTGAAAAT ACACTTATTT	2308
CAGCCAAAAC ATACCATTTC TACACCTCAA TCCTCCATTT GCTGTACTCT TTGCTAGTAC	2368
CAAAAGTAGA CTGATTACAC TGAGGTGAGG CTACAAGGGG TGTGTAACCG TGTAACACGT	2428
GAAGGCAGTG CTCACCTCTT CTTTACCAGA ACGGTTCTTT GACCAGCACA TTAAC TTCTG	2488
GA CTGCCGGC TCTAGTACCT TTTCAGTAAA GTGGTTCTCT GCCTTTTTTAC TATACAGCAT	2548
ACCACGCCAC AGGGTTAGAA CCAACGAAGA AAATAAAATG AGGGTGCCCA GCTTATAAGA	2608
ATGGTGTTAG GGGGATGAGC ATGCTGTTTA TGAACGGAAA TCATGATTTC CCTGTAGAAA	2668
GTGAGGCTCA GATTAAATTT TAGAATATTT TCTAAATGTC TTTTTCACAA TCATGTGACT	2728
GGGAAGGCAA TTTCATACTA AACTGATTAA ATAATACATT TATAATCTAC AACTGTTTGC	2788
ACTTACAGCT TTTTTTGTA ATATAAACTA TAATTTATTG TCTATTTTAT ATCTGTTTTG	2848
CTGTGGCGTT GGGGGGGGGG CCGGGCTTTT GGGGGGGGGG GTTTGTTTGG GGGGTGTCGT	2908
GGTGTGGGCG GGCGG	2923

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Pro Gly Leu Gly Arg Arg Ala Gln Trp Leu Cys Trp Trp Trp Gly	
-374	-370 -365 -360
Leu Leu Cys Ser Cys Cys Gly Pro Pro Pro Leu Arg Pro Pro Leu Pro	
	-355 -350 -345
Ala Ala Ala Ala Ala Ala Ala Gly Gly Gln Leu Leu Gly Asp Gly Gly	
	-340 -335 -330



Ser Pro Gly Arg Thr Glu Gln Pro Pro Ser Pro Gln Ser Ser Ser  
 -325 -320 -315

Gly Phe Leu Tyr Arg Arg Leu Lys Thr Gln Glu Lys Arg Glu Met Gln  
 -310 -305 -300 -295

Lys Glu Ile Leu Ser Val Leu Gly Leu Pro His Arg Pro Arg Pro Leu  
 -290 -285 -280

His Gly Leu Gln Gln Pro Gln Pro Pro Ala Leu Arg Gln Gln Glu Glu  
 -275 -270 -265

Gln Gln Gln Gln Gln Gln Leu Pro Arg Gly Glu Pro Pro Pro Gly Arg  
 -260 -255 -250

Leu Lys Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr Asn Ala Leu Ser  
 -245 -240 -235

Ala Asp Asn Asp Glu Asp Gly Ala Ser Glu Gly Glu Arg Gln Gln Ser  
 -230 -225 -220 -215

Trp Pro His Glu Ala Ala Ser Ser Ser Gln Arg Arg Gln Pro Pro Pro  
 -210 -205 -200

Gly Ala Ala His Pro Leu Asn Arg Lys Ser Leu Leu Ala Pro Gly Ser  
 -195 -190 -185

Gly Ser Gly Gly Ala Ser Pro Leu Thr Ser Ala Gln Asp Ser Ala Phe  
 -180 -175 -170

Leu Asn Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu Tyr  
 -165 -160 -155

Asp Lys Glu Phe Ser Pro Arg Gln Arg His His Lys Glu Phe Lys Phe  
 -150 -145 -140 -135

Asn Leu Ser Gln Ile Pro Glu Gly Glu Val Val Thr Ala Ala Glu Phe  
 -130 -125 -120

Arg Ile Tyr Lys Asp Cys Val Met Gly Ser Phe Lys Asn Gln Thr Phe  
 -115 -110 -105

Leu Ile Ser Ile Tyr Gln Val Leu Gln Glu His Gln His Arg Asp Ser  
 -100 -95 -90

Asp Leu Phe Leu Leu Asp Thr Arg Val Val Trp Ala Ser Glu Glu Gly  
 -85 -80 -75

Trp Leu Glu Phe Asp Ile Thr Ala Thr Ser Asn Leu Trp Val Val Thr  
 -70 -65 -60 -55

Pro Gln His Asn Met Gly Leu Gln Leu Ser Val Val Thr Arg Asp Gly  
 -50 -45 -40

Val His Val His Pro Arg Ala Ala Gly Leu Val Gly Arg Asp Gly Pro  
 -35 -30 -25

Tyr Asp Lys Gln Pro Phe Met Val Ala Phe Phe Lys Val Ser Glu Val  
 -20 -15 -10

His Val Arg Thr Thr Arg Ser Ala Ser Ser Arg Arg Arg Gln Gln Ser  
 -5 1 5 10  
 Arg Asn Arg Ser Thr Gln Ser Gln Asp Val Ala Arg Val Ser Ser Ala  
 15 20 25  
 Ser Asp Tyr Asn Ser Ser Glu Leu Lys Thr Ala Cys Arg Lys His Glu  
 30 35 40  
 Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala  
 45 50 55  
 Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp Gly Glu Cys Ser Phe Pro  
 60 65 70  
 Leu Asn Ala His Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu  
 75 80 85 90  
 Val His Leu Met Asn Pro Glu Tyr Val Pro Lys Pro Cys Cys Ala Pro  
 95 100 105  
 Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Asn Ser Asn  
 110 115 120  
 Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys  
 125 130 135  
 His

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (H) CELL LINE: U2-OS osteosarcoma

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: U2-OS human osteosarcoma cDNA library
- (B) CLONE: U2-16

(viii) POSITION IN GENOME:

- (C) UNITS: bp

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 699..2063

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1647..2060

(ix) FEATURE:

(A) NAME/KEY: mRNA

(B) LOCATION: 1..2153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTGGTATATT TGTGCCTGCT GGAGGTGGAA TTAACAGTAA GAAGGAGAAA GGGATTGAAT	60
GGACTTACAG GAAGGATTTC AAGTAAATTC AGGGAAACAC ATTTACTTGA ATAGTACAAC	120
CTAGAGTATT ATTTTACACT AAGACGACAC AAAAGATGTT AAAGTTATCA CCAAGCTGCC	180
GGACAGATAT ATATTCCAAC ACCAAGGTGC AGATCAGCAT AGATCTGTGA TTCAGAAATC	240
AGGATTTGTT TTGGAAAGAG CTCAAGGGTT GAGAAGAACT CAAAAGCAAG TGAAGATTAC	300
TTTGCGAACT ACAGTTTATC AGAAGATCAA CTTTGTCTAA TTCAAATACC AAAGGCCTGA	360
TTATCATAAA TTCATATAGG AATGCATAGG TCATCTGATC AAATAATATT AGCCGTCTTC	420
TGCTACATCA ATGCAGCAAA AACTCTTAAC AACTGTGGAT AATTGGAAAT CTGAGTTTCA	480
GCTTTCTTAG AAATAACTAC TCTTGACATA TTCCAAAATA TTTAAAATAG GACAGGAAAA	540
TCGGTGAGGA TGTGTGCTC AGAAATGTCA CTGTCATGAA AAATAGGTAA ATTTGTTTTT	600
TCAGCTACTG GGAAACTGTA CCTCCTAGAA CCTTAGGTTT TTTTTTTTTT AAGAGGACAA	660
GAAGGACTAA AAATATCAAC TTTTGCTTTT GGACAAAA ATG CAT CTG ACT GTA	713
Met His Leu Thr Val	
-316-315	
TTT TTA CTT AAG GGT ATT GTG GGT TTC CTC TGG AGC TGC TGG GTT CTA	761
Phe Leu Leu Lys Gly Ile Val Gly Phe Leu Trp Ser Cys Trp Val Leu	
-310 -305 -300	
GTG GGT TAT GCA AAA GGA GGT TTG GGA GAC AAT CAT GTT CAC TCC AGT	809
Val Gly Tyr Ala Lys Gly Gly Leu Gly Asp Asn His Val His Ser Ser	
-295 -290 -285 -280	
TTT ATT TAT AGA AGA CTA CGG AAC CAC GAA AGA CGG GAA ATA CAA AGG	857
Phe Ile Tyr Arg Arg Leu Arg Asn His Glu Arg Arg Glu Ile Gln Arg	
-275 -270 -265	
GAA ATT CTC TCT ATC TTG GGT TTG CCT CAC AGA CCC AGA CCA TTT TCA	905
Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg Pro Arg Pro Phe Ser	
-260 -255 -250	
CCT GGA AAA ATG ACC AAT CAA GCG TCC TCT GCA CCT CTC TTT ATG CTG	953
Pro Gly Lys Met Thr Asn Gln Ala Ser Ser Ala Pro Leu Phe Met Leu	
-245 -240 -235	
GAT CTC TAC AAT GCC GAA GAA AAT CCT GAA GAG TCG GAG TAC TCA GTA	1001
Asp Leu Tyr Asn Ala Glu Glu Asn Pro Glu Glu Ser Glu Tyr Ser Val	
-230 -225 -220	
AGG GCA TCC TTG GCA GAA GAG ACC AGA GGG GCA AGA AAG GGA TAC CCA	1049
Arg Ala Ser Leu Ala Glu Glu Thr Arg Gly Ala Arg Lys Gly Tyr Pro	
-215 -210 -205 -200	

GCC TCT CCC AAT GGG TAT CCT CGT CGC ATA CAG TTA TCT CGG ACG ACT	1097
Ala Ser Pro Asn Gly Tyr Pro Arg Arg Ile Gln Leu Ser Arg Thr Thr	
-195 -190 -185	
CCT CTG ACC ACC CAG AGT CCT CCT CTA GCC AGC CTC CAT GAT ACC AAC	1145
Pro Leu Thr Thr Gln Ser Pro Pro Leu Ala Ser Leu His Asp Thr Asn	
-180 -175 -170	
TTT CTG AAT GAT GCT GAC ATG GTC ATG AGC TTT GTC AAC TTA GTT GAA	1193
Phe Leu Asn Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu	
-165 -160 -155	
AGA GAC AAG GAT TTT TCT CAC CAG CGA AGG CAT TAC AAA GAA TTT CGA	1241
Arg Asp Lys Asp Phe Ser His Gln Arg Arg His Tyr Lys Glu Phe Arg	
-150 -145 -140	
TTT GAT CTT ACC CAA ATT CCT CAT GGA GAG GCA GTG ACA GCA GCT GAA	1289
Phe Asp Leu Thr Gln Ile Pro His Gly Glu Ala Val Thr Ala Ala Glu	
-135 -130 -125 -120	
TTC CGG ATA TAC AAG GAC CGG AGC AAC AAC CGA TTT GAA AAT GAA ACA	1337
Phe Arg Ile Tyr Lys Asp Arg Ser Asn Asn Arg Phe Glu Asn Glu Thr	
-115 -110 -105	
ATT AAG ATT AGC ATA TAT CAA ATC ATC AAG GAA TAC ACA AAT AGG GAT	1385
Ile Lys Ile Ser Ile Tyr Gln Ile Ile Lys Glu Tyr Thr Asn Arg Asp	
-100 -95 -90	
GCA GAT CTG TTC TTG TTA GAC ACA AGA AAG GCC CAA GCT TTA GAT GTG	1433
Ala Asp Leu Phe Leu Leu Asp Thr Arg Lys Ala Gln Ala Leu Asp Val	
-85 -80 -75	
GGT TGG CTT GTC TTT GAT ATC ACT GTG ACC AGC AAT CAT TGG GTG ATT	1481
Gly Trp Leu Val Phe Asp Ile Thr Val Thr Ser Asn His Trp Val Ile	
-70 -65 -60	
AAT CCC CAG AAT AAT TTG GGC TTA CAG CTC TGT GCA GAA ACA GGG GAT	1529
Asn Pro Gln Asn Asn Leu Gly Leu Gln Leu Cys Ala Glu Thr Gly Asp	
-55 -50 -45 -40	
GGA CGC AGT ATC AAC GTA AAA TCT GCT GGT CTT GTG GGA AGA CAG GGA	1577
Gly Arg Ser Ile Asn Val Lys Ser Ala Gly Leu Val Gly Arg Gln Gly	
-35 -30 -25	
CCT CAG TCA AAA CAA CCA TTC ATG GTG GCC TTC TTC AAG GCG AGT GAG	1625
Pro Gln Ser Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Ser Glu	
-20 -15 -10	
GTA CTT CTT CGA TCC GTG AGA GCA GCC AAC AAA CGA AAA AAT CAA AAC	1673
Val Leu Leu Arg Ser Val Arg Ala Ala Asn Lys Arg Lys Asn Gln Asn	
-5 1 5	
CGC AAT AAA TCC AGC TCT CAT CAG GAC TCC TCC AGA ATG TCC AGT GTT	1721
Arg Asn Lys Ser Ser Ser His Gln Asp Ser Ser Arg Met Ser Ser Val	
10 15 20 25	
GGA GAT TAT AAC ACA AGT GAG CAA AAA CAA GCC TGT AAG AAG CAC GAA	1769
Gly Asp Tyr Asn Thr Ser Glu Gln Lys Gln Ala Cys Lys Lys His Glu	
30 35 40	

CTC TAT GTG AGC TTC CGG GAT CTG GGA TGG CAG GAC TGG ATT ATA GCA	1817
Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala	
45 50 55	
CCA GAA GGA TAC GCT GCA TTT TAT TGT GAT GGA GAA TGT TCT TTT CCA	1865
Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp Gly Glu Cys Ser Phe Pro	
60 65 70	
CTT AAC GCC CAT ATG AAT GCC ACC AAC CAC GCT ATA GTT CAG ACT CTG	1913
Leu Asn Ala His Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu	
75 80 85	
GTT CAT CTG ATG TTT CCT GAC CAC GTA CCA AAG CCT TGT TGT GCT CCA	1961
Val His Leu Met Phe Pro Asp His Val Pro Lys Pro Cys Cys Ala Pro	
90 95 100 105	
ACC AAA TTA AAT GCC ATC TCT GTT CTG TAC TTT GAT GAC AGC TCC AAT	2009
Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn	
110 115 120	
GTC ATT TTG AAA AAA TAT AGA AAT ATG GTA GTA CGC TCA TGT GGC TGC	2057
Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ser Cys Gly Cys	
125 130 135	
CAC TAATATTAAA TAATATTGAT AATAACAAAA AGATCTGTAT TAAGGTTTAT	2110
His	
GGCTGCAATA AAAAGCATAC TTTCAGACAA ACAGAAAAAA AAA	2153

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met His Leu Thr Val Phe Leu Leu Lys Gly Ile Val Gly Phe Leu Trp	
-316 -315 -310 -305	
Ser Cys Trp Val Leu Val Gly Tyr Ala Lys Gly Gly Leu Gly Asp Asn	
-300 -295 -290 -285	
His Val His Ser Ser Phe Ile Tyr Arg Arg Leu Arg Asn His Glu Arg	
-280 -275 -270	
Arg Glu Ile Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg	
-265 -260 -255	
Pro Arg Pro Phe Ser Pro Gly Lys Met Thr Asn Gln Ala Ser Ser Ala	
-250 -245 -240	
Pro Leu Phe Met Leu Asp Leu Tyr Asn Ala Glu Glu Asn Pro Glu Glu	
-235 -230 -225	

Ser Glu Tyr Ser Val Arg Ala Ser Leu Ala Glu Glu Thr Arg Gly Ala  
 -220 -215 -210 -205  
 Arg Lys Gly Tyr Pro Ala Ser Pro Asn Gly Tyr Pro Arg Arg Ile Gln  
 -200 -195 -190  
 Leu Ser Arg Thr Thr Pro Leu Thr Thr Gln Ser Pro Pro Leu Ala Ser  
 -185 -180 -175  
 Leu His Asp Thr Asn Phe Leu Asn Asp Ala Asp Met Val Met Ser Phe  
 -170 -165 -160  
 Val Asn Leu Val Glu Arg Asp Lys Asp Phe Ser His Gln Arg Arg His  
 -155 -150 -145  
 Tyr Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro His Gly Glu Ala  
 -140 -135 -130 -125  
 Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp Arg Ser Asn Asn Arg  
 -120 -115 -110  
 Phe Glu Asn Glu Thr Ile Lys Ile Ser Ile Tyr Gln Ile Ile Lys Glu  
 -105 -100 -95  
 Tyr Thr Asn Arg Asp Ala Asp Leu Phe Leu Leu Asp Thr Arg Lys Ala  
 -90 -85 -80  
 Gln Ala Leu Asp Val Gly Trp Leu Val Phe Asp Ile Thr Val Thr Ser  
 -75 -70 -65  
 Asn His Trp Val Ile Asn Pro Gln Asn Asn Leu Gly Leu Gln Leu Cys  
 -60 -55 -50 -45  
 Ala Glu Thr Gly Asp Gly Arg Ser Ile Asn Val Lys Ser Ala Gly Leu  
 -40 -35 -30  
 Val Gly Arg Gln Gly Pro Gln Ser Lys Gln Pro Phe Met Val Ala Phe  
 -25 -20 -15  
 Phe Lys Ala Ser Glu Val Leu Leu Arg Ser Val Arg Ala Ala Asn Lys  
 -10 -5 1  
 Arg Lys Asn Gln Asn Arg Asn Lys Ser Ser Ser His Gln Asp Ser Ser  
 5 10 15 20  
 Arg Met Ser Ser Val Gly Asp Tyr Asn Thr Ser Glu Gln Lys Gln Ala  
 25 30 35  
 Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln  
 40 45 50  
 Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp Gly  
 55 60 65  
 Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala  
 70 75 80  
 Ile Val Gln Thr Leu Val His Leu Met Phe Pro Asp His Val Pro Lys  
 85 90 95 100

Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe  
105 110 115

Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val  
120 125 130

Arg Ser Cys Gly Cys His  
135

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1003 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
  - (F) TISSUE TYPE: Human Heart
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: Human heart cDNA library stratagene catalog  
#936208
  - (B) CLONE: hh38
- (viii) POSITION IN GENOME:
  - (C) UNITS: bp
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 8..850
- (ix) FEATURE:
  - (A) NAME/KEY: mat\_peptide
  - (B) LOCATION: 427..843
- (ix) FEATURE:
  - (A) NAME/KEY: mRNA
  - (B) LOCATION: 1..997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAATTCC	GAG	CCC	CAT	TGG	AAG	GAG	TTC	CGC	TTT	GAC	CTG	ACC	CAG	ATC	49	
	Glu	Pro	His	Trp	Lys	Glu	Phe	Arg	Phe	Asp	Leu	Thr	Gln	Ile		
	-139				-135					-130						
CCG	GCT	GGG	GAG	GCG	GTC	ACA	GCT	GCG	GAG	TTC	CGG	ATT	TAC	AAG	GTG	97
Pro	Ala	Gly	Glu	Ala	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile	Tyr	Lys	Val	
-125					-120					-115					-110	
CCC	AGC	ATC	CAC	CTG	CTC	AAC	AGG	ACC	CTC	CAC	GTC	AGC	ATG	TTC	CAG	145
Pro	Ser	Ile	His	Leu	Leu	Asn	Arg	Thr	Leu	His	Val	Ser	Met	Phe	Gln	

-105

-100

-95

GTG	GTC	CAG	GAG	CAG	TCC	AAC	AGG	GAG	TCT	GAC	TTG	TTC	TTT	TTG	GAT	193
Val	Val	Gln	Glu	Gln	Ser	Asn	Arg	Glu	Ser	Asp	Leu	Phe	Phe	Leu	Asp	
		-90						-85					-80			
CTT	CAG	ACG	CTC	CGA	GCT	GGA	GAC	GAG	GGC	TGG	CTG	GTG	CTG	GAT	GTC	241
Leu	Gln	Thr	Leu	Arg	Ala	Gly	Asp	Glu	Gly	Trp	Leu	Val	Leu	Asp	Val	
		-75					-70					-65				
ACA	GCA	GCC	AGT	GAC	TGC	TGG	TTG	CTG	AAG	CGT	CAC	AAG	GAC	CTG	GGA	289
Thr	Ala	Ala	Ser	Asp	Cys	Trp	Leu	Leu	Lys	Arg	His	Lys	Asp	Leu	Gly	
	-60					-55				-50						
CTC	CGC	CTC	TAT	GTG	GAG	ACT	GAG	GAT	GGG	CAC	AGC	GTG	GAT	CCT	GGC	337
Leu	Arg	Leu	Tyr	Val	Glu	Thr	Glu	Asp	Gly	His	Ser	Val	Asp	Pro	Gly	
	-45				-40				-35						-30	
CTG	GCC	GGC	CTG	CTG	GGT	CAA	CGG	GCC	CCA	CGC	TCC	CAA	CAG	CCT	TTC	385
Leu	Ala	Gly	Leu	Leu	Gly	Gln	Arg	Ala	Pro	Arg	Ser	Gln	Gln	Pro	Phe	
				-25				-20						-15		
GTG	GTC	ACT	TTC	TTC	AGG	GCC	AGT	CCG	AGT	CCC	ATC	CGC	ACC	CCT	CGG	433
Val	Val	Thr	Phe	Phe	Arg	Ala	Ser	Pro	Ser	Pro	Ile	Arg	Thr	Pro	Arg	
		-10					-5						1			
GCA	GTG	AGG	CCA	CTG	AGG	AGG	AGG	CAG	CCG	AAG	AAA	AGC	AAC	GAG	CTG	481
Ala	Val	Arg	Pro	Leu	Arg	Arg	Arg	Gln	Pro	Lys	Lys	Ser	Asn	Glu	Leu	
	5					10					15					
CCG	CAG	GCC	AAC	CGA	CTC	CCA	GGG	ATC	TTT	GAT	GAC	GTC	CAC	GGC	TCC	529
Pro	Gln	Ala	Asn	Arg	Leu	Pro	Gly	Ile	Phe	Asp	Asp	Val	His	Gly	Ser	
	20				25					30					35	
CAC	GGC	CGG	CAG	GTC	TGC	CGT	CGG	CAC	GAG	CTC	TAC	GTC	AGC	TTC	CAG	577
His	Gly	Arg	Gln	Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val	Ser	Phe	Gln	
			40						45					50		
GAC	CTT	GGC	TGG	CTG	GAC	TGG	GTC	ATC	GCC	CCC	CAA	GGC	TAC	TCA	GCC	625
Asp	Leu	Gly	Trp	Leu	Asp	Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser	Ala	
			55					60					65			
TAT	TAC	TGT	GAG	GGG	GAG	TGC	TCC	TTC	CCG	CTG	GAC	TCC	TGC	ATG	AAC	673
Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ser	Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	
		70					75					80				
GCC	ACC	AAC	CAC	GCC	ATC	CTG	CAG	TCC	CTG	GTG	CAC	CTG	ATG	AAG	CCA	721
Ala	Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu	Val	His	Leu	Met	Lys	Pro	
	85					90					95					
AAC	GCA	GTC	CCC	AAG	GCG	TGC	TGT	GCA	CCC	ACC	AAG	CTG	AGC	GCC	ACC	769
Asn	Ala	Val	Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys	Leu	Ser	Ala	Thr	
	100				105				110					115		
TCT	GTG	CTC	TAC	TAT	GAC	AGC	AGC	AAC	AAC	GTC	ATC	CTG	CGC	AAG	CAC	817
Ser	Val	Leu	Tyr	Tyr	Asp	Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg	Lys	His	
			120					125						130		
CGC	AAC	ATG	GTG	GTC	AAG	GCC	TGC	GGC	TGC	CAC	TGAGTCAGCC	CGCCCAGCCC				870
Arg	Asn	Met	Val	Val	Lys	Ala	Cys	Gly	Cys	His						



TACTGCAGCC ACCCTTCTCA TCTGGATCGG GCCCTGCAGA GGCAGAAAAC CCTTAAATGC 930  
 TGTCACAGCT CAAGCAGGAG TGTGAGGGGC CCTCACTCTC GGTGCCTACT TCCTGTCAGG 990  
 CTTCTGGGAA TTC 1003

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Glu Pro His Trp Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro Ala  
 -139 -135 -130 -125  
 Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val Pro Ser  
 -120 -115 -110  
 Ile His Leu Leu Asn Arg Thr Leu His Val Ser Met Phe Gln Val Val  
 -105 -100 -95  
 Gln Glu Gln Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln  
 -90 -85 -80  
 Thr Leu Arg Ala Gly Asp Glu Gly Trp Leu Val Leu Asp Val Thr Ala  
 -75 -70 -65 -60  
 Ala Ser Asp Cys Trp Leu Leu Lys Arg His Lys Asp Leu Gly Leu Arg  
 -55 -50 -45  
 Leu Tyr Val Glu Thr Glu Asp Gly His Ser Val Asp Pro Gly Leu Ala  
 -40 -35 -30  
 Gly Leu Leu Gly Gln Arg Ala Pro Arg Ser Gln Gln Pro Phe Val Val  
 -25 -20 -15  
 Thr Phe Phe Arg Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg Ala Val  
 -10 -5 1 5  
 Arg Pro Leu Arg Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln  
 10 15 20  
 Ala Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His Gly Ser His Gly  
 25 30 35  
 Arg Gln Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu  
 40 45 50  
 Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr  
 55 60 65  
 Cys Glu Gly Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr

Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala  
                     90                    95                    100

Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val  
                     105                    110                    115

Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn  
                     120                    125                    130

Met Val Val Lys Ala Cys Gly Cys His  
                     135                    140

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3623 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: pALBP2-781

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2724..3071

(ix) FEATURE:

- (A) NAME/KEY: terminator
- (B) LOCATION: 3150..3218

(ix) FEATURE:

- (A) NAME/KEY: RBS
- (B) LOCATION: 2222..2723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GACGAAAGGG CCTCGTGATA CGCCTATTTT TATAGGTAA TGTCATGATA ATAATGGTTT	60
CTTAGACGTC AGGTGGCACT TTTCGGGGAA ATGTGCGCGG AACCCCTATT TGTTTATTTT	120
TCTAAATACA TTCAAATATG TATCCGCTCA TGAGACAATA ACCCTGATAA ATGCTTCAAT	180
AATATTGAAA AAGGAAGAGT ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT	240
TTGCGGCATT TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG	300
CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC AGCGGTAAGA	360
TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT GAGCACTTTT AAAGTTCTGC	420
TATGTGGCGC GGTATTATCC CGTATTGACG CCGGGCAAGA GCAACTCGGT CGCCGCATAC	480
ACTATTCTCA GAATGACTTG GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG	540

GCATGACAGT AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA 600

ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTTG CACAACATGG 660

GGGATCATGT AACTCGCCTT GATCGTTGGG AACC GGAGCT GAATGAAGCC ATACCAAACG 720

ACGAGCGTGA CACCACGATG CCTGTAGCAA TGGCAACAAC GTTGC GCAA CTATTAACTG 780

GCGAACTACT TACTCTAGCT TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG 840

TTGCAGGACC ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG 900

GAGCCGGTGA GCGTGGGTCT CGCGGTATCA TTGCAGCACT GGGGCCAGAT GGTAAGCCCT 960

CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC TATGGATGAA CGAAATAGAC 1020

AGATCGCTGA GATAGGTGCC TCACTGATTA AGCATTGGTA ACTGTCAGAC CAAGTTTACT 1080

CATATATACT TTAGATTGAT TTA AAACTTC ATTTT TAATT TAAAAGGATC TAGGTGAAGA 1140

TCCTTTTTGA TAATCTCATG ACCAAAATCC CTTAACGTGA GTTTTCGTTT CACTGAGCGT 1200

CAGACCCCGT AGAAAAGATC AAAGGATCTT CTTGAGATCC TTTTTTCTG CGCGTAATCT 1260

GCTGCTTGCA AACAAAAAAA CCACCGCTAC CAGCGGTGGT TTGTTTGCCG GATCAAGAGC 1320

TACCAACTCT TTTTCCGAAG GTA ACTGGCT TCAGCAGAGC GCAGATACCA AATACTGTCC 1380

TTCTAGTGTA GCCGTAGTTA GGCCACCACT TCAAGAACTC TG TAGCACCG CCTACATACC 1440

TCGCTCTGCT AATCCTGTTA CCAGTGGCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG 1500

GGTTGGA CT AAGACGATAG TTACCGGATA AGGCGCAGCG GTCGGGCTGA ACGGGGGGTT 1560

CGTGACACA GCCCAGCTTG GAGCGAACGA CCTACACCGA ACTGAGATAC CTACAGCGTG 1620

AGCATTGAGA AAGCGCCACG CTTCCCGAAG GGAGAAAGGC GGACAGGTAT CCGGTAAGCG 1680

GCAGGGTCGG AACAGGAGAG CGCACGAGGG AGCTTCCAGG GGGAAACGCC TGGTATCTTT 1740

ATAGTCCTGT CGGGTTTCGC CACCTCTGAC TTGAGCGTCG ATTTTGTGA TGCTCGTCAG 1800

GGGGGCGGAG CCTATGAAA AACGCCAGCA ACGCGGCCTT TTTACGGTTC CTGGCCTTTT 1860

GCTGGCCTTT TGCTCACATG TTCTTTCCTG CGTTATCCCC TGATTCTGTG GATAACCGTA 1920

TTACCGCCTT TGAGTGAGCT GATACCGCTC GCCGCAGCCG AACGACCGAG CGCAGCGAGT 1980

CAGTGAGCGA GGAAGCGGAA GAGCGCCCAA TACGCAAACC GCCTCTCCCC GCGCGTTGGC 2040

CGATTCATTA ATGCAGAATT GATCTCTCAC CTACCAAACA ATGCCCCCT GCAAAAATA 2100

AATTCATATA AAAAACATAC AGATAACCAT CTGCGGTGAT AAATTATCTC TGGCGGTGTT 2160

GACATAAATA CCACTGGCGG TGATACTGAG CACATCAGCA GGACGCACTG ACCACCATGA 2220

AGGTGACGCT CTAAAAAATT AAGCCCTGAA GAAGGGCAGC ATTCAAAGCA GAAGGCTTTG 2280

GGGTGTGTGA TACGAAACGA AGCATTGGCC GTAAGTGCGA TTCCGGATTA GCTGCCAATG 2340

TGCCAATCGC GGGGGGTTTT CGTTCAGGAC TACAAC TGCC ACACACCACC AAAGCTAACT	2400
GACAGGAGAA TCCAGATGGA TGCACAAACA CGCCGCCGCG AACGTCGCGC AGAGAAACAG	2460
GCTCAATGGA AAGCAGCAAA TCCCCTGTTG GTTGGGGTAA GCGCAAAACC AGTTCCGAAA	2520
GATTTTTTTTA ACTATAAACG CTGATGGAAG CGTTTATGCG GAAGAGGTAA AGCCCTTCCC	2580
GAGTAACAAA AAAACAACAG CATAAATAAC CCCGCTCTTA CACATTCCAG CCCTGAAAAA	2640
GGGCATCAAA TTAAACCACA CCTATGGTGT ATGCATTTAT TTGCATACAT TCAATCAATT	2700
GTTATCTAAG GAAATACTTA CAT ATG CAA GCT AAA CAT AAA CAA CGT AAA	2750
Met Gln Ala Lys His Lys Gln Arg Lys	
1 5	
CGT CTG AAA TCT AGC TGT AAG AGA CAC CCT TTG TAC GTG GAC TTC AGT	2798
Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu Tyr Val Asp Phe Ser	
10 15 20 25	
GAC GTG GGG TGG AAT GAC TGG ATT GTG GCT CCC CCG GGG TAT CAC GCC	2846
Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr His Ala	
30 35 40	
TTT TAC TGC CAC GGA GAA TGC CCT TTT CCT CTG GCT GAT CAT CTG AAC	2894
Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His Leu Asn	
45 50 55	
TCC ACT AAT CAT GCC ATT GTT CAG ACG TTG GTC AAC TCT GTT AAC TCT	2942
Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser	
60 65 70	
AAG ATT CCT AAG GCA TGC TGT GTC CCG ACA GAA CTC AGT GCT ATC TCG	2990
Lys Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser	
75 80 85	
ATG CTG TAC CTT GAC GAG AAT GAA AAG GTT GTA TTA AAG AAC TAT CAG	3038
Met Leu Tyr Leu Asp Glu Asn Glu Lys Val Val Leu Lys Asn Tyr Gln	
90 95 100 105	
GAC ATG GTT GTG GAG GGT TGT GGG TGT CGC TAGTACAGCA AAATTAAATA	3088
Asp Met Val Val Glu Gly Cys Gly Cys Arg	
110 115	
CATAAATATA TATATATATA TATATTTTAG AAAAAAGAAA AAAATCTAGA GTCGACCTGC	3148
AGTAATCGTA CAGGGTAGTA CAAATAAAAA AGGCACGTCA GATGACGTGC CTTTTTCTT	3208
GTGAGCAGTA AGCTTGGCAC TGGCCGTCGT TTTACAACGT CGTGACTGGG AAAACCCTGG	3268
CGTTACCCAA CTTAATCGCC TTGCAGCACA TCCCCCTTTC GCCAGCTGGC GTAATAGCGA	3328
AGAGGCCCGC ACCGATCGCC CTTCCCAACA GTTGCGCAGC CTGAATGGCG AATGGCGCCT	3388
GATGCGGTAT TTTCTCCTTA CGCATCTGTG CGGTATTTCA CACCGCATAT ATGGTGCACT	3448
CTCAGTACAA TCTGCTCTGA TGCCGCATAG TTAAGCCAGC CCCGACACCC GCCAACACCC	3508
GCTGACGCGC CCTGACGGGC TTGTCTGCTC CCGGCATCCG CTTACAGACA AGCTGTGACC	3568

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

Met Gln Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys Lys
 1             5             10             15
Arg His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp
      20             25             30
Ile Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu Cys
      35             40             45
Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Val
      50             55             60
Gln Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys
      65             70             75             80
Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn
      85             90             95
Glu Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu Gly Cys
      100            105            110
Gly Cys Arg
      115

```

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CATGGGCAGC TGAG

14

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAGGGTTGTG GGTGTCGCTA GTGAGTCGAC TACAGCAAAT T

41

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGATGTGGGT GCCGCTGACT CTAGAGTCGA CGGAATTC

38

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AATTCACCAT GATTCTGGT AACCGAATGC T

31

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTGGTACTAA GGACCATGG CTTAC

25

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CGACCTGCAG CCATGCATCT GACTGTA

27

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TGCCTGCAGT TTAATATTAG TGGCAGC

27

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGACCTGCAG CCACC

15

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 81 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TCGACCCACC ATGCCGGGGC TGGGGCGGAG GCGCAGTGG CTGTGCTGCT GGTGGGGGCT 60  
GTGCTGCAGC TGCTGCGGGC C 81

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGCAGCAGCT GCACAGCAGC CCCCACCACC AGCACAGCCA CTGCGCCCTC CGCCCCAGCC 60  
CCGGCATGGT GGG 73

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TCGACTGGTT T 11

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CGAAACCAG 9

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs



(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCGACAGGCT CGCCTGCA

18

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTCCGAGCGG

10

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAGGTCGACC CACCATGCAC GTGCGCTCA

29

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TCTGTCGACC TCGGAGGAGC TAGTGGC

27

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1794 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: bmp-3

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 321..1136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AGATCTTGAA AACACCCGGG CCACACACGC CGCGACCTAC AGCTCTTTCT CAGCGTTGGA	60
GTGGAGACGG CGCCCGCAGC GCCCTGCGCG GGTGAGGTCC GCGCAGCTGC TGGGGAAGAG	120
CCCACCTGTC AGGCTGCGCT GGGTCAGCGC AGCAAGTGGG GCTGGCCGCT ATCTCGCTGC	180
ACCCGGCCGC GTCCCGGGCT CCGTGC GCCC TCGCCCCAGC TGGTTTGGAG TTCAACCCCTC	240
GGCTCCGCCG CCGGCTCCTT GCGCCTTCGG AGTGTCCCGC AGCGACGCCG GGAGCCGACG	300
CGCCGCGCGG GTACCTAGCC ATG GCT GGG GCG AGC AGG CTG CTC TTT CTG	350
Met Ala Gly Ala Ser Arg Leu Leu Phe Leu	
1 5 10	
TGG CTG GGC TGC TTC TGC GTG AGC CTG GCG CAG GGA GAG AGA CCG AAG	398
Trp Leu Gly Cys Phe Cys Val Ser Leu Ala Gln Gly Glu Arg Pro Lys	
15 20 25	
CCA CCT TTC CCG GAG CTC CGC AAA GCT GTG CCA GGT GAC CGC ACG GCA	446
Pro Pro Phe Pro Glu Leu Arg Lys Ala Val Pro Gly Asp Arg Thr Ala	
30 35 40	
GGT GGT GGC CCG GAC TCC GAG CTG CAG CCG CAA GAC AAG GTC TCT GAA	494
Gly Gly Gly Pro Asp Ser Glu Leu Gln Pro Gln Asp Lys Val Ser Glu	
45 50 55	
CAC ATG CTG CGG CTC TAT GAC AGG TAC AGC ACG GTC CAG GCG GCC CGG	542
His Met Leu Arg Leu Tyr Asp Arg Tyr Ser Thr Val Gln Ala Ala Arg	
60 65 70	
ACA CCG GGC TCC CTG GAG GGA GGC TCG CAG CCC TGG CGC CCT CGG CTC	590
Thr Pro Gly Ser Leu Glu Gly Gly Ser Gln Pro Trp Arg Pro Arg Leu	
75 80 85 90	
CTG CGC GAA GGC AAC ACG GTT CGC AGC TTT CGG GCG GCA GCA GCA GAA	638
Leu Arg Glu Gly Asn Thr Val Arg Ser Phe Arg Ala Ala Ala Ala Glu	
95 100 105	
ACT CTT GAA AGA AAA GGA CTG TAT ATC TTC AAT CTG ACA TCG CTA ACC	686
Thr Leu Glu Arg Lys Gly Leu Tyr Ile Phe Asn Leu Thr Ser Leu Thr	
110 115 120	

AAG TCT GAA AAC ATT TTG TCT GCC ACA CTG TAT TTC TGT ATT GGA GAG Lys Ser Glu Asn Ile Leu Ser Ala Thr Leu Tyr Phe Cys Ile Gly Glu 125 130 135	734
CTA GGA AAC ATC AGC CTG AGT TGT CCA GTG TCT GGA GGA TGC TCC CAT Leu Gly Asn Ile Ser Leu Ser Cys Pro Val Ser Gly Gly Cys Ser His 140 145 150	782
CAT GCT CAG AGG AAA CAC ATT CAG ATT GAT CTT TCT GCA TGG ACC CTC His Ala Gln Arg Lys His Ile Gln Ile Asp Leu Ser Ala Trp Thr Leu 155 160 165 170	830
AAA TTC AGC AGA AAC CAA AGT CAA CTC CTT GGC CAT CTG TCA GTG GAT Lys Phe Ser Arg Asn Gln Ser Gln Leu Leu Gly His Leu Ser Val Asp 175 180 185	878
ATG GCC AAA TCT CAT CGA GAT ATT ATG TCC TGG CTG TCT AAA GAT ATC Met Ala Lys Ser His Arg Asp Ile Met Ser Trp Leu Ser Lys Asp Ile 190 195 200	926
ACT CAA TTC TTG AGG AAG GCC AAA GAA AAT GAA GAG TTC CTC ATA GGA Thr Gln Phe Leu Arg Lys Ala Lys Glu Asn Glu Glu Phe Leu Ile Gly 205 210 215	974
TTT AAC ATT ACG TCC AAG GGA CGC CAG CTG CCA AAG AGG AGG TTA CCT Phe Asn Ile Thr Ser Lys Gly Arg Gln Leu Pro Lys Arg Arg Leu Pro 220 225 230	1022
TTT CCA GAG CCT TAT ATC TTG GTA TAT GCC AAT GAT GCC GCC ATT TCT Phe Pro Glu Pro Tyr Ile Leu Val Tyr Ala Asn Asp Ala Ala Ile Ser 235 240 245 250	1070
GAG CCA GAA AGT GTG GTA TCA AGC TTA CAG GGA CAC CGG AAT TTT CCC Glu Pro Glu Ser Val Val Ser Ser Leu Gln Gly His Arg Asn Phe Pro 255 260 265	1118
ACT GGA ACT GTT CCC AAA TGGGATAGCC ACATCAGAGC TGCCCTTTCC Thr Gly Thr Val Pro Lys 270	1166
ATTGAGCGGA GGAAGAAGCG CTCTACTGGG GTCTTGCTGC CTCTGCAGAA CAACGAGCTT	1226
CCTGGGGCAG AATACCAGTA TAAAAAGGAT GAGGTGTGGG AGGAGAGAAA GCCTTACAAG	1286
ACCCTTCAGG CTCAGGCCCC TGAAAAGAGT AAGAATAAAA AGAAACAGAG AAAGGGGCCT	1346
CATCGGAAGA GCCAGACGCT CCAATTTGAT GAGCAGACCC TGAAAAAGGC AAGGAGAAAG	1406
CAGTGGATTG AACCTCGGAA TTGCGCCAGG AGATACCTCA AGGTAGACTT TGCAGATATT	1466
GGCTGGAGTG AATGGATTAT CTCCCCAAG TCCTTTGATG CCTATTATTG CTCTGGAGCA	1526
TGCCAGTTCC CCATGCCAAA GTCTTTGAAG CCATCAAATC ATGCTACCAT CCAGAGTATA	1586
GTGAGAGCTG TGGGGGTCGT TCCTGGGATT CCTGAGCCTT GCTGTGTACC AGAAAAGATG	1646
TCCTCACTCA GTATTTTATT CTTTGATGAA AATAAGAATG TAGTGCTTAA AGTATACCCT	1706
AACATGACAG TAGAGTCTTG CGCTTGCAGA TAACCTGGCA AAGAACTCAT TTGAATGCTT	1766

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

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Met Ala Gly Ala Ser Arg Leu Leu Phe Leu Trp Leu Gly Cys Phe Cys
 1           5           10           15
Val Ser Leu Ala Gln Gly Glu Arg Pro Lys Pro Pro Phe Pro Glu Leu
          20           25           30
Arg Lys Ala Val Pro Gly Asp Arg Thr Ala Gly Gly Gly Pro Asp Ser
          35           40           45
Glu Leu Gln Pro Gln Asp Lys Val Ser Glu His Met Leu Arg Leu Tyr
          50           55           60
Asp Arg Tyr Ser Thr Val Gln Ala Ala Arg Thr Pro Gly Ser Leu Glu
          65           70           75           80
Gly Gly Ser Gln Pro Trp Arg Pro Arg Leu Leu Arg Glu Gly Asn Thr
          85           90           95
Val Arg Ser Phe Arg Ala Ala Ala Ala Glu Thr Leu Glu Arg Lys Gly
          100          105          110
Leu Tyr Ile Phe Asn Leu Thr Ser Leu Thr Lys Ser Glu Asn Ile Leu
          115          120          125
Ser Ala Thr Leu Tyr Phe Cys Ile Gly Glu Leu Gly Asn Ile Ser Leu
          130          135          140
Ser Cys Pro Val Ser Gly Gly Cys Ser His His Ala Gln Arg Lys His
          145          150          155          160
Ile Gln Ile Asp Leu Ser Ala Trp Thr Leu Lys Phe Ser Arg Asn Gln
          165          170          175
Ser Gln Leu Leu Gly His Leu Ser Val Asp Met Ala Lys Ser His Arg
          180          185          190
Asp Ile Met Ser Trp Leu Ser Lys Asp Ile Thr Gln Phe Leu Arg Lys
          195          200          205
Ala Lys Glu Asn Glu Glu Phe Leu Ile Gly Phe Asn Ile Thr Ser Lys
          210          215          220
Gly Arg Gln Leu Pro Lys Arg Arg Leu Pro Phe Pro Glu Pro Tyr Ile
          225          230          235          240

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Leu Val Tyr Ala Asn Asp Ala Ala Ile Ser Glu Pro Glu Ser Val Val  
 245 250 255

Ser Ser Leu Gln Gly His Arg Asn Phe Pro Thr Gly Thr Val Pro Lys  
 260 265 270

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 449 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGTCTCATA ATCGTTCTAA AACTCCAAAA AATCAAGAAG CTCTGCGTAT GGCCAACGTG	60
GCAGAGAACA GCAGCAGCGA CCAGAGGCAG GCCTGTAAGA AGCACGAGCT GTATGTCAGC	120
TTCCGAGACC TGGGCTGGCA GGACTGGATC ATCGCGCCTG AAGGCTACGC CGCCTACTAC	180
TGTGAGGGGG AGTGTGCCTT CCCTCTGAAC TCCTACATGA ACGCCACCAA CCACGCCATC	240
GTGCAGACGC TGGTCCACTT CATCAACCCG GAAACGGTGC CCAAGCCCTG CTGTGCGCCC	300
ACGCAGCTCA ATGCCATCTC CGTCCTCTAC TTCGATGACA GCTCCAACGT CATCCTGAAG	360
AAATACAGAA ACATGGTGGT CCGGGCCTGT GGCTGCCACT AGCTCCTCCG AGAATTCAGA	420
CCCTTTGGGG CCAAGTTTTT CTGGATCCT	449

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CAAGAAGGAG ATATACAT	18
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(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 377 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATGCGTAAAC AATGGATTGA ACCACGTAAC TGTGCTCGTC GTTATCTGAA AGTAGACTTT	60
GCAGATATTG GCTGGAGTGA ATGGATTATC TCCCCCAAGT CCTTTGATGC CTATTATTGC	120
TCTGGAGCAT GCCAGTTCCC CATGCCAAAG TCTTTGAAGC CATCAAATCA TGCTACCATC	180
CAGAGTATAG TGAGAGCTGT GGGGGTCGTT CCTGGGATTC CTGAGCCTTG CTGTGTACCA	240
GAAAAGATGT CCTCACTCAG TATTTTATTC TTTGATGAAA ATAAGAATGT AGTGCTTAAA	300
GTATACCCTA ACATGACAGT AGAGTCTTGC GCTTGCAGAT AACCTGGCAA AGAACTCATT	360
TGAATGCTTA ATTCAAT	377